AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

LISTING OF CLAIMS

Claims 1-11 (withdrawn)

Claim 12 (Previously Amended) A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is a gene product whose activity or amount is reduced by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claims 13-30 (withdrawn)

Claim 31 (Previously Amended) A method for screening a candidate compound for the ability to reduce cellular proliferation comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the

group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a nonsensitized cell.

Claims 32-44 (withdrawn)

Claim 45 (Previously Added) The method of Claim 31, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 46 (Previously Added) The method of Claim 31, wherein said gene product is from an organism other than *E. coli*.

Claim 47 (Previously Added) The method of Claim 31, wherein said cell is an organism other than *E. coli*.

Claim 48 (Currently Amended) The method of Claim 31, wherein said sensitized cell is a pathogenic microorganism ~~an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium diffieile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escheriehia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium ieprae, Mycobacterium tuberculosis,*~~

~~*Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis*~~ ~~and any species falling within the genera of any of the above species~~.

Claim 49 **(Previously Added)** The method of Claim 31, wherein said sensitized cell is a Gram positive bacterium.

Claim 50 **(Previously Added)** The method of Claim 49, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 51 **(Previously Added)** The method of Claim 50, wherein said bacterium is *Staphylococcus aureus*.

Claim 52 **(Previously Added)** The method of Claim 50, wherein said *Staphylococcus* species is coagulase negative.

Claim 53 **(Previously Added)** The method of Claim 51, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 54 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 55 **(Previously Added)** The method of Claim 31, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 56 **(Previously Added)** The method of Claim 31, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claim 57 **(Previously Added)** The method of Claim 31, wherein said gene product is a polypeptide.

Claim 58 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 99% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 59 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 95% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 60 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 90% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 61 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 85% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 62 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least at least 80% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide

selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 63 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 70% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 64 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 60% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 65 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 50% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 66 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 40% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide

selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 67 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 68 **(Previously Added)** The method of Claim 57, wherein said polypeptide is selected from the group consisting of 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 69 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 34% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 39% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 42% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600 and a polypeptide having at least 43% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600.

Claim 70 **(Previously Added)** The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 32% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689, a polypeptide having at least 33% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689, a polypeptide having at least 37% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689, a polypeptide having at least 63% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689 and a polypeptide having at least 77% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689.

Claim 71 **(Previously Added)** The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 97% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 72 **(Previously Added)** The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 95% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 73 **(Previously Added)** The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 90% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 74 **(Previously Added)** The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 85% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 75 **(Previously Added)** The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 80% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 76 **(Previously Added)** The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 77 **(Previously Added)** The method of Claim 31, wherein said nucleic acid encoding said gene product is selected from the group consisting of 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605.

Claim 78 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 97% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 79 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 95% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 80 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 90% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 81 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 85% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 82 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 80% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 83 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 84 **(Previously Added)** The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence comprising at least 100 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283.

Claim 85 **(Previously Added)** The method of Claim 12, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 86 **(Previously Added)** The method of Claim 12, wherein said gene product is from an organism other than *E. coli*.

Claim 87 **(Previously Added)** The method of Claim 12, wherein said cell is an organism other than *E. coli*.

Claim 88 **(Amended)** The method of Claim 12, wherein said sensitized cell is a pathogenic microorganism ~~an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species~~.

Claim 89 **(Previously Added)** The method of Claim 12, wherein said sensitized cell is a Gram positive bacterium.

Claim 90 **(Previously Added)** The method of Claim 89, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus*

species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 91 **(Previously Added)** The method of Claim 90, wherein said bacterium is *Staphylococcus aureus*.

Claim 92 **(Previously Added)** The method of Claim 90, wherein said *Staphylococcus* species is coagulase negative.

Claim 93 **(Previously Added)** The method of Claim 91, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 94 **(Previously Added)** The method of Claim 12, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 95 **(Previously Added)** The method of Claim 12, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 96 **(Previously Added)** The method of Claim 12, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claim 97 **(Previously Added)** The method of Claim 12, wherein said gene product is a polypeptide.

Claim 98 **(Previously Added)** The method of Claim 97, wherein said polypeptide is selected from the group consisting of 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 99 **(Previously Added)** The method of Claim 12, wherein said nucleic acid encoding said gene product is selected from the group consisting of 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605.

Claim 100 **(Previously Added)** A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283, wherein said antisense nucleic acid reduces the activity or amount of a gene product required for cellular proliferation, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claim 101 (New) The method of Claim 48, wherein said pathogenic mircoorganism is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

Claim 102 (New) The method of Claim 88, wherein said pathogenic microorganism is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes,*

Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.